

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Gregor Meyers, Tillmann Rümenapf,
Heinz-Jürgen Thiel
- (ii) TITLE OF INVENTION: Hog cholera virus vaccine and diagnostic
- (iii) NUMBER OF SEQUENCES: 13
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: Organon Teknika Corporation
Biotechnology Research Institute
 - (B) STREET: 1330-A Piccard Drive
 - (C) CITY: Rockville
 - (D) STATE: Maryland
 - (E) COUNTRY: U.S.A.
 - (F) ZIP: 20850
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: US 494,991
 - (B) FILING DATE: 16 March 1990
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: William M. Blackstone
 - (B) REGISTRATION NUMBER: 29,772
 - (C) REFERENCE/DOCKET NUMBER:
- (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: (301) 258-5200

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12284 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Hog cholera virus
- (B) STRAIN: Alfort
- (H) CELL LINE: PK 15 and 38A1D

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 364..12060
- (D) OTHER INFORMATION: /label= 435_kDA_protein

(ix) FEATURE:

- (A) NAME/KEY: primer_bind
- (B) LOCATION: complement (2587..2619)
- (D) OTHER INFORMATION: /label= primer_1

(ix) FEATURE:

- (A) NAME/KEY: primer_bind
- (B) LOCATION: complement (2842..2880)
- (D) OTHER INFORMATION: /label= primer_2

(ix) FEATURE:

- (A) NAME/KEY: variation
- (B) LOCATION: replace(127, "c")

(ix) FEATURE:

- (A) NAME/KEY: variation
- (B) LOCATION: replace(1522, "g")

(ix) FEATURE:

- (A) NAME/KEY: variation
- (B) LOCATION: replace(10989, "t")

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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CTAGCCGTAG TGGCGAGCTC CCTGGGTGGT CTAAGTCCTG AGTACAGGAC AGTCGTCAGT   180
AGTTCGACGT GAGCACTAGC CCACCTCGAG ATGCTACGTG GACGAGGGCA TGCCCAAGAC   240
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AAA CCA GTG GGA GTG GAG GAA CCG GTG TAT GAC ACC GCG GGG AGA CCA Lys Pro Val Gly Val Glu Glu Pro Val Tyr Asp Thr Ala Gly Arg Pro 20 25 30	456
CTA TTT GGG AAC CCA AGT GAG GTA CAC CCA CAA TCA ACG CTG AAG CTG Leu Phe Gly Asn Pro Ser Glu Val His Pro Gln Ser Thr Leu Lys Leu 35 40 45	504
CCA CAC GAC AGG GGG AGA GGA GAT ATC AGA ACA ACA CTG AGG GAC CTA Pro His Asp Arg Gly Arg Gly Asp Ile Arg Thr Thr Leu Arg Asp Leu 50 55 60	552
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TGC GAG GTG ACT AAG AGA ATA GGC AGG GTC ACG GGT AGT GAT GGT AAG Cys Glu Val Thr Lys Arg Ile Gly Arg Val Thr Gly Ser Asp Gly Lys 115 120 125	744
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GTC Val	AAA Lys 225	GGG Gly	AAG Lys	AAC Asn	ACA Thr 230	CAA Gln	GAC Asp	GGC Gly	CTG Leu	TAC Tyr	CAT His 235	AAT Asn	AAG Lys	AAC Asn	AAG Lys	1080
CCA Pro 240	CCA Pro	GAG Glu	TCC Ser	AGG Arg	AAG Lys 245	AAA Lys	CTA Leu	GAA Glu	AAA Lys 250	GCC Ala	CTG Leu	TTG Leu	GCT Ala	TGG Trp	GCG Ala 255	1128
GTG Val	ATA Ile	ACA Thr	ATC Ile	TTG Leu 260	CTG Leu	TAC Tyr	CAG Gln	CCT Pro	GTA Val 265	GCA Ala	GCC Ala	GAG Glu	AAC Asn	ATA Ile 270	ACT Thr	1176
CAA Gln	TGG Trp	AAC Asn 275	CTG Leu	AGT Ser	GAC Asp	AAC Asn	GGC Gly	ACT Thr 280	AAT Asn	GGT Gly	ATT Ile	CAG Gln	CGA Arg	GCC Ala	ATG Met	1224
TAT Tyr	CTT Leu	AGA Arg 290	GGG Gly	GTT Val	AAC Asn	AGG Arg	AGC Ser 295	TTA Leu	CAT His	GGG Gly	ATC Ile	TGG Trp 300	CCC Pro	GAG Glu	AAA Lys	1272
ATA Ile	TGC Cys 305	AAG Lys	GGG Gly	GTC Val	CCC Pro	ACT Thr 310	CAT His	CTG Leu	GCC Ala	ACT Thr	GAC Asp 315	ACG Thr	GAA Glu	CTG Leu	AAA Lys	1320
GAG Glu 320	ATA Ile	CGC Arg	GGG Gly	ATG Met	ATG Met	GAT Asp	GCC Ala	AGC Ser	GAG Glu	AGG Arg	ACA Thr	AAC Asn	TAT Tyr	ACG Thr	TGC Cys 335	1368
TGT Cys	AGG Arg	TTA Leu	CAA Gln	AGA Arg	CAT His	GAA Glu	TGG Trp	AAC Asn	AAA Lys 345	CAT His	GGA Gly	TGG Trp	TGT Cys	AAC Asn	TGG Trp	1416
TAC Tyr	AAC Asn	ATA Ile	GAC Asp	CCT Pro	TGG Trp	ATT Ile	CAG Gln	TTA Leu	ATG Met	AAC Asn	AGG Arg	ACC Thr	CAA Gln	ACA Thr	AAT Asn	1464
TTG Leu	ACA Thr 370	GAA Glu	GGC Gly	CCT Pro	CCA Pro	GAT Asp	AAG Lys 375	GAG Glu	TGT Cys	GCC Ala	GTG Val	ACC Thr	TGC Cys	AGG Arg	TAT Tyr	1512
GAC Asp	AAA Lys 385	AAT Asn	ACC Thr	GAT Asp	GTC Val	AAC Asn	GTG Val	GTC Val	ACC Thr	CAG Gln	GCC Ala	AGG Arg	AAT Asn	AGG Arg	CCA Pro	1560
ACT Thr 400	ACT Thr	CTG Leu	ACT Thr	GGC Gly	TGC Cys 405	AAG Lys	AAA Lys	GGG Gly	AAA Lys	AAC Asn 410	TTT Phe	TCA Ser	TTC Phe	GCA Ala	GGC Gly 415	1608
ACA Thr	GTC Val	ATA Ile	GAG Glu	GGC Gly 420	CCG Pro	TGC Cys	AAT Asn	TTC Phe	AAC Asn 425	GTT Val	TCC Ser	GTG Val	GAG Glu	GAC Asp	ATC Ile 430	1656

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640 645 650 655	

35

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GGA	CAG	GTT	GTG	CAA	GGT	ATA	ATA	TGG	CTG	CTG	CTG	GTG	ACC	GGG	GCA	2424
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Thr	Asn	Glu	Ile	Gly	Leu	Leu	Gly	Ala	Glu	Gly	Leu	Thr	Thr	Thr	Trp	
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Val	Cys	Thr	Ala	Gly	Ser	Phe	Lys	Val	Thr	Ala	Leu	Asn	Val	Val	Ser	
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CTA	GTC	TGC	CCA	ATA	GGA	TGG	ACT	GGT	GTC	GTA	GAG	TGC	ACA	GCA	GTG	2856
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Ser	Pro	Thr	Thr	Leu	Arg	Thr	Glu	Val	Val	Lys	Thr	Phe	Arg	Arg	Asp	
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GAG Glu 945	TGC Cys 945	TTG Leu 945	ATT Ile 945	GGC Gly 950	AAC Asn 950	ACT Thr 950	ACC Thr 950	GTC Val 950	AAG Lys 950	GTG Val 955	CAT His 955	GCA Ala 955	CTG Leu 955	GAT Asp 955	GAA Glu 955	3240
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CTC Leu 1010	AAG Lys 1010	GGC Gly 1010	GAG Glu 1010	TAT Tyr 1010	CAA Gln 1010	TAC Tyr 1015	TGG Trp 1015	TTT Phe 1015	AAT Asn 1015	CTG Leu 1015	GAC Asp 1020	GTG Val 1020	ACC Thr 1020	GAC Asp 1020	CAC His 1020	3432
CAC His 1025	ACA Thr 1025	GAC Asp 1025	TAC Tyr 1025	TTT Phe 1025	GCC Ala 1030	GAG Glu 1030	TTT Phe 1030	GTT Val 1030	GTC Val 1030	TTG Leu 1035	GTA Val 1035	GTA Val 1035	GTA Val 1035	GCA Ala 1035	CTG Leu 1035	3480
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GAT Asp	GGT Gly	GGC Gly	TGG Trp	CAG Gln	AGA Arg	CAA Gln	CCG Pro	GTG Val	ACC Thr	AGT Ser	TTT Phe	GAC Asp	ATC Ile	CAA Gln	CTC Leu	3816
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GCA Ala	CTG Leu	GCA Ala	GTC Val	GTA Val	GTA Val	GTC Val	GTT Val	GTG Val	ATG Met	TTG Leu	CTG Leu	GCA Ala	AAG Lys	AGA Arg	GAC Asp	3864
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AGG Arg	GTG Val	CTG Leu	AAG Lys	GGA Gly	ATA Ile	GGC Gly	GAA Glu	TTG Leu	GAT Asp	CTG Leu	CAC His	GCC Ala	CCA Pro	ACC Thr	TTG Leu	4104
			1235					1240				1245				
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GCC Ala	GTG Val	GTA Val	ACT Thr	AGA Arg	TGG Trp	AAT Asn	CTG Leu	GAC Asp	GTA Val	GCC Ala	GGA Gly	TTG Leu	TTG Leu	CTG Leu	CAG Gln	4200
	1265					1270					1275					
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ACC Thr	CTA Leu	ATT Ile	CTC Leu	ATA Ile	CTA Leu	CCT Pro	ACT Thr	TAT Tyr	GAG Glu	TTA Leu	ACA Thr	AAG Lys	TTA Leu	TAC Tyr	TAC Tyr	4296
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CTT Leu	AAG Lys	GAA Glu	GTG Val	AAG Lys	ATT Ile	GGG Gly	GCA Ala	GAA Glu	AGA Arg	GGT Gly	TGG Trp	CTG Leu	TGG Trp	AAA Lys	ACT Thr	4344
			1315					1320				1325				

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ACC Thr	ATG Met	TTG Leu	CCA Pro	TTA Leu	ATC Ile	AAA Lys	GCC Ala	ATA Ile	CTC Leu	ATT Ile	AGC Ser	TGC Cys	ATC Ile	AGC Ser	AAC Asn	4488
		1360					1365				1370					1375
AAG Lys	TGG Trp	CAA Gln	CTC Leu	ATA Ile	TAC Tyr	TTA Leu	CTG Leu	TAC Tyr	TTG Leu	ATA Ile	TTT Phe	GAA Glu	GTG Val	TCT Ser	TAC Tyr	4536
				1380						1385					1390	
TAC Tyr	CTC Leu	CAC His	AAG Lys	AAA Lys	GTT Val	ATA Ile	GAT Asp	GAA Glu	ATA Ile	GCT Ala	GGT Gly	GGG Gly	ACC Thr	AAC Asn	TTC Phe	4584
				1395					1400					1405		
GTT Val	TCA Ser	AGG Arg	CTC Leu	GTG Val	GCG Ala	GCT Ala	TTG Leu	ATT Ile	GAA Glu	GTC Val	AAT Asn	TGG Trp	GCC Ala	TTC Phe	GAC Asp	4632
		1410					1415					1420				
AAT Asn	GAA Glu	GAA Glu	GTC Val	AAA Lys	GGC Gly	TTA Leu	AAG Lys	AAG Lys	TTC Phe	TTC Phe	TTG Leu	CTG Leu	TCT Ser	AGT Ser	AGG Arg	4680
		1425					1430					1435				
GTC Val	AAA Lys	GAG Glu	TTG Leu	ATC Ile	ATC Ile	AAA Lys	CAC His	AAA Lys	GTG Val	AGG Arg	AAT Asn	GAA Glu	GTA Val	GTG Val	GTC Val	4728
		1440				1445				1450					1455	
CGC Arg	TGG Trp	TTT Phe	GGA Gly	GAT Asp	GAA Glu	GAG Glu	ATT Ile	TAT Tyr	GGG Gly	ATG Met	CCA Pro	AAG Lys	CTG Leu	ATC Ile	GGC Gly	4776
				1460						1465					1470	
TTA Leu	GTT Val	AAG Lys	GCA Ala	GCA Ala	ACA Thr	CTA Leu	AGT Ser	AGA Arg	AAC Asn	AAA Lys	CAC His	TGT Cys	ATG Met	TTG Leu	TGT Cys	4824
				1475					1480				1485			
ACC Thr	GTC Val	TGT Cys	GAG Glu	GAC Asp	AGA Arg	GAT Asp	TGG Trp	AGA Arg	GGG Gly	GAA Glu	ACT Thr	TGC Cys	CCT Pro	AAA Lys	TGT Cys	4872
		1490					1495						1500			
GGG Gly	CGT Arg	TTT Phe	GGA Gly	CCA Pro	CCA Pro	GTG Val	GTC Val	TGC Cys	GGT Gly	ATG Met	ACC Thr	CTA Leu	GCC Ala	GAT Asp	TTC Phe	4920
		1505					1510					1515				
GAA Glu	GAA Glu	AAA Lys	CAC His	TAT Tyr	AAA Lys	AGG Arg	ATT Ile	TTC Phe	ATT Ile	AGA Arg	GAG Glu	GAC Asp	CAA Gln	TCA Ser	GGC Gly	4968
		1520				1525				1530					1535	
GGG Gly	CCA Pro	CTT Leu	AGG Arg	GAG Glu	GAG Glu	CAT His	GCA Ala	GGG Gly	TAC Tyr	TTG Leu	CAG Gln	TAC Tyr	AAA Lys	GCC Ala	AGG Arg	5016
				1540					1545					1550		

GGT CAA CTG TTT TTG AGG AAC CTC CCA GTG TTA GCT ACA AAA GTC AAG Gly Gln Leu Phe Leu Arg Asn Leu Pro Val Leu Ala Thr Lys Val Lys 1555 1560 1565	5064
ATG CTC CTG GTT GGT AAC CTC GGG ACA GAG ATT GGG GAT CTG GAA CAC Met Leu Leu Val Gly Asn Leu Gly Thr Glu Ile Gly Asp Leu Glu His 1570 1575 1580	5112
CTT GGC TGG GTG CTT AGA GGG CCA GCT GTT TGC AAG AAG GTT ACT GAA Leu Gly Trp Val Leu Arg Gly Pro Ala Val Cys Lys Lys Val Thr Glu 1585 1590 1595	5160
CAC GAA AGA TGC ACC ACG TCT ATA ATG GAT AAG TTG ACT GCT TTC TTT His Glu Arg Cys Thr Thr Ser Ile Met Asp Lys Leu Thr Ala Phe Phe 1600 1605 1610 1615	5208
GGA GTA ATG CCA AGG GGC ACT ACT CCC AGA GCT CCC GTA AGA TTC CCT Gly Val Met Pro Arg Gly Thr Thr Pro Arg Ala Pro Val Arg Phe Pro 1620 1625 1630	5256
ACC TCC CTC CTA AAG ATA AGA AGA GGG CTG GAG ACT GGT TGG GCT TAC Thr Ser Leu Leu Lys Ile Arg Arg Gly Leu Glu Thr Gly Trp Ala Tyr 1635 1640 1645	5304
ACA CAC CAA GGT GGC ATC AGC TCA GTA GAC CAT GTC ACT TGT GGG AAA Thr His Gln Gly Gly Ile Ser Ser Val Asp His Val Thr Cys Gly Lys 1650 1655 1660	5352
GAC TTA CTG GTG TGT GAC ACC ATG GGT CGG ACA AGG GTT GTT TGC CAG Asp Leu Leu Val Cys Asp Thr Met Gly Arg Thr Arg Val Val Cys Gln 1665 1670 1675	5400
TCA AAT AAT AAG ATG ACC GAC GAG TCC GAA TAC GGA GTC AAA ACT GAC Ser Asn Asn Lys Met Thr Asp Glu Ser Glu Tyr Gly Val Lys Thr Asp 1680 1685 1690 1695	5448
TCC GGG TGC CCA GAG GGA GCC AGG TGT TAC GTG TTT AAC CCG GAA GCA Ser Gly Cys Pro Glu Gly Ala Arg Cys Tyr Val Phe Asn Pro Glu Ala 1700 1705 1710	5496
GTT AAC ATA TCA GGC ACT AAA GGA GCC ATG GTC CAC TTA CAG AAA ACG Val Asn Ile Ser Gly Thr Lys Gly Ala Met Val His Leu Gln Lys Thr 1715 1720 1725	5544
GGT GGA GAA TTC ACC TGT GTG ACA GCA TCA GGA ACC CCG GCC TTC TTT Gly Gly Glu Phe Thr Cys Val Thr Ala Ser Gly Thr Pro Ala Phe Phe 1730 1735 1740	5592
GAC CTC AAG AAC CTT AAG GGC TGG TCA GGG CTA CCG ATA TTT GAA GCA Asp Leu Lys Asn Leu Lys Gly Trp Ser Gly Leu Pro Ile Phe Glu Ala 1745 1750 1755	5640
TCA AGT GGA AGG GTA GTC GGA AGG GTC AAG GTC GGG AAG AAC GAG GAT Ser Ser Gly Arg Val Val Gly Arg Val Lys Val Gly Lys Asn Glu Asp 1760 1765 1770 1775	5688

TCC AAA CCA ACC AAG CTC ATG AGT GGG ATA CAA ACG GTT TCT AAA AGC Ser Lys Pro Thr Lys Leu Met Ser Gly Ile Gln Thr Val Ser Lys Ser 1780 1785 1790	5736
GCC ACA GAC TTG ACG GAG ATG GTG AAG AAG ATA ACG ACC ATG AAC AGG Ala Thr Asp Leu Thr Glu Met Val Lys Lys Ile Thr Thr Met Asn Arg 1795 1800 1805	5784
GGA GAG TTC AGA CAA ATA ACC CTG GCC ACA GGT GCC GGA AAA ACT ACA Gly Glu Phe Arg Gln Ile Thr Leu Ala Thr Gly Ala Gly Lys Thr Thr 1810 1815 1820	5832
GAG CTC CCT AGA TCA GTT ATA GAA GAG ATA GGG AGG CAT AAG AGG GTG Glu Leu Pro Arg Ser Val Ile Glu Glu Ile Gly Arg His Lys Arg Val 1825 1830 1835	5880
TTG GTC TTA ATC CCC TTG AGG GCG GCA GCA GAA TCA GTA TAC CAA TAC Leu Val Leu Ile Pro Leu Arg Ala Ala Ala Glu Ser Val Tyr Gln Tyr 1840 1845 1850 1855	5928
ATG AGA CAG AAA CAT CCG AGT ATA GCA TTC AAT CTA AGG ATA GGT GAG Met Arg Gln Lys His Pro Ser Ile Ala Phe Asn Leu Arg Ile Gly Glu 1860 1865 1870	5976
ATG AAG GAA GGT GAT ATG GCC ACG GGA ATA ACC TAT GCC TCT TAC GGT Met Lys Glu Gly Asp Met Ala Thr Gly Ile Thr Tyr Ala Ser Tyr Gly 1875 1880 1885	6024
TAC TTT TGC CAG ATG TCA CAA CCC AAG CTG AGA GCC GCA ATG GTA GAA Tyr Phe Cys Gln Met Ser Gln Pro Lys Leu Arg Ala Ala Met Val Glu 1890 1895 1900	6072
TAT TCC TTT ATA TTC CTA GAT GAG TAT CAT TGT GCT ACC CCA GAA CAA Tyr Ser Phe Ile Phe Leu Asp Glu Tyr His Cys Ala Thr Pro Glu Gln 1905 1910 1915	6120
CTG GCA ATC ATG GGG AAG ATC CAC AGA TTC TCA GAA AAC CTG CGG GTG Leu Ala Ile Met Gly Lys Ile His Arg Phe Ser Glu Asn Leu Arg Val 1920 1925 1930 1935	6168
GTA GCT ATG ACA GCG ACA CCG GCA GGC ACA GTA ACA ACC ACT GGG CAG Val Ala Met Thr Ala Thr Pro Ala Gly Thr Val Thr Thr Thr Gly Gln 1940 1945 1950	6216
AAA CAC CCT ATA GAG GAA TTT ATA GCC CCG GAA GTG ATG AAA GGA GAA Lys His Pro Ile Glu Glu Phe Ile Ala Pro Glu Val Met Lys Gly Glu 1955 1960 1965	6264
GAC TTG GGT TCT GAG TAC TTA GAT ATT GCC GGA CTG AAG ATA CCA GTA Asp Leu Gly Ser Glu Tyr Leu Asp Ile Ala Gly Leu Lys Ile Pro Val 1970 1975 1980	6312
GAG GAG ATG AAG AAT AAC ATG CTA GTT TTT GTG CCC ACC AGG AAC ATG Glu Glu Met Lys Asn Asn Met Leu Val Phe Val Pro Thr Arg Asn Met 1985 1990 1995	6360

GCG GTA GAG GCG GCA AAG AAA TTG AAG GCC AAA GGA TAC AAC TCG GGC Ala Val Glu Ala Ala Lys Lys Leu Lys Ala Lys Gly Tyr Asn Ser Gly 2000 2005 2010 2015	6408
TAC TAC TAC AGC GGA GAG GAC CCA TCT AAC CTG AGG GTG GTG ACG TCG Tyr Tyr Tyr Ser Gly Glu Asp Pro Ser Asn Leu Arg Val Val Thr Ser 2020 2025 2030	6456
CAG TCC CCA TAC GTG GTG GTA GCA ACC AAC GCA ATA GAA TCG GGC GTT Gln Ser Pro Tyr Val Val Val Ala Thr Asn Ala Ile Glu Ser Gly Val 2035 2040 2045	6504
ACC CTC CCG GAC CTG GAC GTG GTT GTC GAC ACG GGA CTC AAG TGT GAA Thr Leu Pro Asp Leu Asp Val Val Val Asp Thr Gly Leu Lys Cys Glu 2050 2055 2060	6552
AAA AGA ATC CGA CTG TCA CCC AAG ATG CCT TTC ATA GTG ACG GGC CTG Lys Arg Ile Arg Leu Ser Pro Lys Met Pro Phe Ile Val Thr Gly Leu 2065 2070 2075	6600
AAA AGA ATG GCC GTC ACT ATT GGG GAA CAA GCC CAG AGA AGA GGG AGG Lys Arg Met Ala Val Thr Ile Gly Glu Gln Ala Gln Arg Arg Gly Arg 2080 2085 2090 2095	6648
GTT GGA AGA GTG AAG CCC GGG AGA TAC TAC AGG AGT CAA GAA ACA CCT Val Gly Arg Val Lys Pro Gly Arg Tyr Tyr Arg Ser Gln Glu Thr Pro 2100 2105 2110	6696
GTC GGC TCT AAA GAC TAC CAT TAT GAC TTA TTG CAA GCC CAG AGG TAC Val Gly Ser Lys Asp Tyr His Tyr Asp Leu Leu Gln Ala Gln Arg Tyr 2115 2120 2125	6744
GGC ATA GAA GAT GGG ATA AAT ATC ACC AAA TCC TTC AGA GAG ATG AAC Gly Ile Glu Asp Gly Ile Asn Ile Thr Lys Ser Phe Arg Glu Met Asn 2130 2135 2140	6792
TAC GAC TGG AGC CTT TAT GAG GAA GAT AGC CTG ATG ATC ACA CAA CTG Tyr Asp Trp Ser Leu Tyr Glu Glu Asp Ser Leu Met Ile Thr Gln Leu 2145 2150 2155	6840
GAA ATC CTC AAC AAC CTG TTG ATA TCA GAA GAG CTG CCG ATG GCA GTA Glu Ile Leu Asn Asn Leu Leu Ile Ser Glu Glu Leu Pro Met Ala Val 2160 2165 2170 2175	6888
AAA AAT ATA ATG GCC AGG ACC GAC CAC CCA GAA CCA ATT CAA CTC GCG Lys Asn Ile Met Ala Arg Thr Asp His Pro Glu Pro Ile Gln Leu Ala 2180 2185 2190	6936
TAT AAC AGC TAC GAG ACA CAG GTG CCG GTA TTA TTC CCA AAA ATA AGA Tyr Asn Ser Tyr Glu Thr Gln Val Pro Val Leu Phe Pro Lys Ile Arg 2195 2200 2205	6984
AAT GGA GAG GTG ACT GAT ACT TAC GAT AAT TAC ACC TTC CTC AAT GCA Asn Gly Glu Val Thr Asp Thr Tyr Asp Asn Tyr Thr Phe Leu Asn Ala 2210 2215 2220	7032

AGA AAA TTG GGA GAT GAC GTA CCC CCC TAC GTG TAT GCT ACA GAG GAT Arg Lys Leu Gly Asp Asp Val Pro Pro Tyr Val Tyr Ala Thr Glu Asp 2225 2230 2235	7080
GAG GAC TTG GCA GTG GAA CTG TTG GGC CTA GAT TGG CCG GAC CCA GGA Glu Asp Leu Ala Val Glu Leu Leu Gly Leu Asp Trp Pro Asp Pro Gly 2240 2245 2250 2255	7128
AAC CAA GGC ACC GTG GAA GCT GGC AGA GCA CTA AAA CAG GTG GTT GGT Asn Gln Gly Thr Val Glu Ala Gly Arg Ala Leu Lys Gln Val Val Gly 2260 2265 2270	7176
CTA TCA ACA GCA GAG AAC GCC CTG CTA GTC GCC CTG TTC GGC TAC GTG Leu Ser Thr Ala Glu Asn Ala Leu Leu Val Ala Leu Phe Gly Tyr Val 2275 2280 2285	7224
GGG TAC CAG GCG CTT TCA AAG AGA CAT ATA CCA GTG GTC ACA GAT ATA Gly Tyr Gln Ala Leu Ser Lys Arg His Ile Pro Val Val Thr Asp Ile 2290 2295 2300	7272
TAT TCA GTA GAA GAT CAC AGG CTA GAG GAC ACT ACG CAC CTA CAG TAT Tyr Ser Val Glu Asp His Arg Leu Glu Asp Thr Thr His Leu Gln Tyr 2305 2310 2315	7320
GCT CCG AAT GCC ATC AAG ACG GAG GGG AAG GAA ACT GAA TTG AAG GAG Ala Pro Asn Ala Ile Lys Thr Glu Gly Lys Glu Thr Glu Leu Lys Glu 2320 2325 2330 2335	7368
CTG GCT CAG GGG GAT GTG CAG AGA TGT GTG GAA GCA GTG ACC AAT TAT Leu Ala Gln Gly Asp Val Gln Arg Cys Val Glu Ala Val Thr Asn Tyr 2340 2345 2350	7416
GCG AGA GAG GGC ATC CAA TTC ATG AAG TCG CAG GCA CTG AAA GTG AGA Ala Arg Glu Gly Ile Gln Phe Met Lys Ser Gln Ala Leu Lys Val Arg 2355 2360 2365	7464
GAA ACC CCT ACC TAT AAA GAG ACA ATG AAC ACC GTG GCA GAT TAT GTG Glu Thr Pro Thr Tyr Lys Glu Thr Met Asn Thr Val Ala Asp Tyr Val 2370 2375 2380	7512
AAA AAG TTT ATT GAG GCA CTG ACG GAT AGC AAG GAA GAC ATC ATT AAA Lys Lys Phe Ile Glu Ala Leu Thr Asp Ser Lys Glu Asp Ile Ile Lys 2385 2390 2395	7560
TAT GGG CTG TGG GGG GCA CAT ACG GCA TTG TAT AAG AGC ATT GGT GCC Tyr Gly Leu Trp Gly Ala His Thr Ala Leu Tyr Lys Ser Ile Gly Ala 2400 2405 2410 2415	7608
AGG CTT GGT CAC GAA ACC GCG TTC GCA ACT CTA GTT GTG AAG TGG TTG Arg Leu Gly His Glu Thr Ala Phe Ala Thr Leu Val Val Lys Trp Leu 2420 2425 2430	7656
GCA TTT GGG GGG GAG TCA ATA TCA GAC CAC ATA AAG CAA GCG GCC ACA Ala Phe Gly Gly Glu Ser Ile Ser Asp His Ile Lys Gln Ala Ala Thr 2435 2440 2445	7704

GAC TTG GTC GTT TAT TAC ATT ATT AAC AGA CCT CAA TTC CCA GGA GAC Asp Leu Val Val Tyr Tyr Ile Ile Asn Arg Pro Gln Phe Pro Gly Asp 2450 2455 2460	7752
ACA GAA ACA CAA CAA GAA GGG AGA AAA TTT GTT GCC AGC CTG CTA GTC Thr Glu Thr Gln Gln Glu Gly Arg Lys Phe Val Ala Ser Leu Leu Val 2465 2470 2475	7800
TCA GCT CTA GCG ACT TAT ACA TAC AAG AGC TGG AAC TAC AAT AAT CTG Ser Ala Leu Ala Thr Tyr Thr Tyr Lys Ser Trp Asn Tyr Asn Asn Leu 2480 2485 2490 2495	7848
TCC AAA ATA GTT GAA CCG GCT TTG GCT ACC CTG CCC TAT GCC GCT AAA Ser Lys Ile Val Glu Pro Ala Leu Ala Thr Leu Pro Tyr Ala Ala Lys 2500 2505 2510	7896
GCC CTC AAG CTA TTT GCT CCT ACC CGA CTG GAG AGC GTT GTC ATA CTG Ala Leu Lys Leu Phe Ala Pro Thr Arg Leu Glu Ser Val Val Ile Leu 2515 2520 2525	7944
AGC ACT GCA ATC TAC AAA ACA TAC CTA TCA ATA AGG CGA GGC AAA AGT Ser Thr Ala Ile Tyr Lys Thr Tyr Leu Ser Ile Arg Arg Gly Lys Ser 2530 2535 2540	7992
GAT GGT CTG CTA GGT ACA GGG GTT AGC GCG GCC ATG GAA ATT ATG TCA Asp Gly Leu Leu Gly Thr Gly Val Ser Ala Ala Met Glu Ile Met Ser 2545 2550 2555	8040
CAA AAC CCA GTA TCT GTG GGT ATA GCA GTT ATG CTA GGG GTA GGG GCT Gln Asn Pro Val Ser Val Gly Ile Ala Val Met Leu Gly Val Gly Ala 2560 2565 2570 2575	8088
GTA GCA GCC CAC AAT GCA ATT GAA GCC AGT GAG CAA AAA AGA ACA CTA Val Ala Ala His Asn Ala Ile Glu Ala Ser Glu Gln Lys Arg Thr Leu 2580 2585 2590	8136
CTT ATG AAA GTC TTT GTG AAA AAC TTC TTA GAC CAG GCC GCC ACC GAC Leu Met Lys Val Phe Val Lys Asn Phe Leu Asp Gln Ala Ala Thr Asp 2595 2600 2605	8184
GAA CTA GTC AAA GAG AGC CCT GAG AAA ATA ATA ATG GCT TTG TTC GAA Glu Leu Val Lys Glu Ser Pro Glu Lys Ile Ile Met Ala Leu Phe Glu 2610 2615 2620	8232
GCG GTG CAA ACG GTG GGC AAC CCT CTT AGA TTA GTG TAC CAC CTC TAT Ala Val Gln Thr Val Gly Asn Pro Leu Arg Leu Val Tyr His Leu Tyr 2625 2630 2635	8280
GGA GTT TTC TAT AAA GGG TGG GAA GCA AAA GAG TTG GCC CAA AGA ACA Gly Val Phe Tyr Lys Gly Trp Glu Ala Lys Glu Leu Ala Gln Arg Thr 2640 2645 2650 2655	8328
GCC GGC AGG AAC CTT TTC ACC TTG ATA ATG TTC GAG GCT GTG GAA CTA Ala Gly Arg Asn Leu Phe Thr Leu Ile Met Phe Glu Ala Val Glu Leu 2660 2665 2670	8376

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CTG	GGA	GTA	GAC	AGT	GAG	GGA	AAA	ATT	CGC	CAG	CTA	TCG	AGC	AAT	TAC	8424
Leu	Gly	Val	Asp	Ser	Glu	Gly	Lys	Ile	Arg	Gln	Leu	Ser	Ser	Asn	Tyr	
			2675					2680					2685			
ATA	CTA	GAG	CTC	TTG	TAT	AAG	TTC	CGC	GAC	AAT	ATC	AAG	TCT	AGT	GTG	8472
Ile	Leu	Glu	Leu	Leu	Tyr	Lys	Phe	Arg	Asp	Asn	Ile	Lys	Ser	Ser	Val	
			2690				2695					2700				
AGG	GAG	ATA	GCA	ATC	AGC	TGG	GCC	CCC	GCC	CCC	TTT	AGT	TGC	GAT	TGG	8520
Arg	Glu	Ile	Ala	Ile	Ser	Trp	Ala	Pro	Ala	Pro	Phe	Ser	Cys	Asp	Trp	
			2705			2710					2715					
ACA	CCA	ACA	GAT	GAC	AGA	ATA	GGG	CTT	CCC	CAT	GAC	AAT	TAC	CTC	CGA	8568
Thr	Pro	Thr	Asp	Asp	Arg	Ile	Gly	Leu	Pro	His	Asp	Asn	Tyr	Leu	Arg	
			2720		2725				2730						2735	
GTG	GAG	ACA	AAG	TGC	CCC	TGT	GGT	TAC	AGG	ATG	AAA	GCG	GTA	AAA	AAC	8616
Val	Glu	Thr	Lys	Cys	Pro	Cys	Gly	Tyr	Arg	Met	Lys	Ala	Val	Lys	Asn	
			2740						2745					2750		
TGC	GCT	GGG	GAG	TTG	AGA	CTT	CTG	GAG	GAA	GGG	GGT	TCA	TTC	CTC	TGC	8664
Cys	Ala	Gly	Glu	Leu	Arg	Leu	Leu	Glu	Glu	Gly	Gly	Ser	Phe	Leu	Cys	
			2755					2760					2765			
AGA	AAT	AAA	TTC	GGT	AGA	GGC	TCA	CAA	AAC	TAC	AGG	GTG	ACA	AAA	TAC	8712
Arg	Asn	Lys	Phe	Gly	Arg	Gly	Ser	Gln	Asn	Tyr	Arg	Val	Thr	Lys	Tyr	
			2770				2775					2780				
TAT	GAT	GAC	AAT	TTA	TCA	GAA	ATA	AAA	CCA	GTG	ATA	AGA	ATG	GAA	GGA	8760
Tyr	Asp	Asp	Asn	Leu	Ser	Glu	Ile	Lys	Pro	Val	Ile	Arg	Met	Glu	Gly	
			2785			2790					2795					
CAC	GTG	GAA	CTG	TAT	TAC	AAG	GGG	GCC	ACT	ATC	AAA	CTG	GAT	TTT	AAC	8808
His	Val	Glu	Leu	Tyr	Tyr	Lys	Gly	Ala	Thr	Ile	Lys	Leu	Asp	Phe	Asn	
			2800		2805				2810						2815	
AAC	AGT	AAA	ACG	GTA	CTG	GCA	ACT	GAC	AAA	TGG	GAG	GTT	GAC	CAC	TCC	8856
Asn	Ser	Lys	Thr	Val	Leu	Ala	Thr	Asp	Lys	Trp	Glu	Val	Asp	His	Ser	
			2820						2825					2830		
ACC	CTG	GTT	AGG	GCA	CTC	AAG	AGG	TAC	ACA	GGG	GCT	GGA	TAT	CGA	GGG	8904
Thr	Leu	Val	Arg	Ala	Leu	Lys	Arg	Tyr	Thr	Gly	Ala	Gly	Tyr	Arg	Gly	
			2835					2840					2845			
GCG	TAT	TTG	GGT	GAG	AAA	CCT	AAC	CAT	AAA	CAT	CTG	ATA	CAG	AGA	GAC	8952
Ala	Tyr	Leu	Gly	Glu	Lys	Pro	Asn	His	Lys	His	Leu	Ile	Gln	Arg	Asp	
			2850			2855						2860				
TGT	GCA	ACG	ATT	ACC	AAA	GAC	AAG	GTC	TGC	TTC	ATC	AAA	ATG	AAG	AGA	9000
Cys	Ala	Thr	Ile	Thr	Lys	Asp	Lys	Val	Cys	Phe	Ile	Lys	Met	Lys	Arg	
			2865			2870					2875					
GGG	TGT	GCG	TTC	ACT	TAT	GAC	CTA	TCC	CTC	CAC	AAC	CTT	ACC	CGG	CTA	9048
Gly	Cys	Ala	Phe	Thr	Tyr	Asp	Leu	Ser	Leu	His	Asn	Leu	Thr	Arg	Leu	
			2880		2885					2890					2895	

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ATC Ile	GAA Glu	TTG Leu	GTA Val	CAC His	AAG Lys	AAT Asn	AAC Asn	CTG Leu	GAA Glu	GAT Asp	AGA Arg	GAA Glu	ATC Ile	CCT Pro	GCT Ala	9096
				2900					2905					2910		
GTG Val	ACG Thr	GTT Val	ACA Thr	ACC Thr	TGG Trp	CTG Leu	GCC Ala	TAC Tyr	ACA Thr	TTT Phe	GTG Val	AAT Asn	GAA Glu	GAC Asp	ATA Ile	9144
				2915				2920						2925		
GGG Gly	ACC Thr	ATA Ile	AAA Lys	CCA Pro	ACT Thr	TTT Phe	GGG Gly	GAA Glu	AAG Lys	GTG Val	ACA Thr	CCG Pro	GAG Glu	AAA Lys	CAG Gln	9192
				2930				2935						2940		
GAG Glu	GAG Glu	GTA Val	GTC Val	TTG Leu	CAG Gln	CCT Pro	GCT Ala	GTG Val	GTG Val	GTG Val	GAC Asp	ACA Thr	ACA Thr	GAT Asp	GTA Val	9240
				2945				2950						2955		
GCC Ala	GTG Val	ACC Thr	GTG Val	GTA Val	GGG Gly	GAA Glu	ACC Thr	TCT Ser	ACT Thr	ATG Met	ACT Thr	ACA Thr	GGG Gly	GAG Glu	ACC Thr	9288
					2960			2965								2975
CCG Pro	ACA Thr	ACA Thr	TTT Phe	ACC Thr	AGC Ser	TTA Leu	GGT Gly	TCG Ser	GAC Asp	TCG Ser	AAG Lys	GTC Val	CGA Arg	CAA Gln	GTC Val	9336
					2980				2985						2990	
CTG Leu	AAG Lys	CTG Leu	GGC Gly	GTG Val	GAC Asp	GAT Asp	GGT Gly	CAA Gln	TAC Tyr	CCC Pro	GGG Gly	CCT Pro	AAT Asn	CAG Gln	CAG Gln	9384
					2995				3000					3005		
AGA Arg	GCA Ala	AGC Ser	CTG Leu	CTC Leu	GAA Glu	GCT Ala	ATA Ile	CAA Gln	GGT Gly	GTG Val	GAT Asp	GAA Glu	AGC Arg	CCC Pro	TCG Ser	9432
					3010			3015						3020		
GTA Val	CTG Leu	ATA Ile	CTG Leu	GGG Gly	TCT Ser	GAT Asp	AAG Lys	GCC Ala	ACC Thr	TCC Ser	AAT Asn	AGG Arg	GTC Val	AAG Lys	ACC Thr	9480
					3025			3030						3035		
GCA Ala	AAG Lys	AAT Asn	GTG Val	AAG Lys	ATA Ile	TAT Tyr	AGG Arg	AGC Ser	AGG Arg	GAC Asp	CCC Pro	CTG Leu	GAA Glu	CTG Leu	AGA Arg	9528
					3040			3045						3050		3055
GAA Glu	ATG Met	ATG Met	AAA Lys	AGG Arg	GGA Gly	AAA Lys	ATC Ile	CTA Leu	GTC Val	GTG Val	GCC Ala	TTG Leu	TCT Ser	AGA Arg	GTC Val	9576
					3060				3065					3070		
GAT Asp	ACC Thr	GCT Ala	CTG Leu	CTG Leu	AAA Lys	TTC Phe	GTT Val	GAT Asp	TAC Tyr	AAA Lys	GGC Gly	ACC Thr	TTC Phe	CTG Leu	ACC Thr	9624
					3075				3080					3085		
AGA Arg	GAG Glu	ACC Thr	CTA Leu	GAG Glu	GCA Ala	TTA Leu	AGT Ser	CTG Leu	GGT Gly	AAG Lys	CCT Pro	AAG Lys	AAA Lys	AGA Arg	GAC Asp	9672
					3090			3095						3100		
ATA Ile	ACT Thr	AAA Lys	GCA Ala	GAA Glu	GCA Ala	CAA Gln	TGG Trp	CTG Leu	CTG Leu	CGC Arg	CTC Leu	GAA Glu	GAC Asp	CAA Gln	ATA Ile	9720
					3105			3110						3115		

GAA GAG CTG CCT GAC TGG TTC GCA GCC AAG GAA CCC ATA TTT CTA GAA Glu Glu Leu Pro Asp Trp Phe Ala Ala Lys Glu Pro Ile Phe Leu Glu 3120 3125 3130 3135	9768
GCC AAC ATT AAA CGT GAC AAG TAT CAC CTG GTA GGG GAC ATA GCC ACT Ala Asn Ile Lys Arg Asp Lys Tyr His Leu Val Gly Asp Ile Ala Thr 3140 3145 3150	9816
ATT AAA GAA AAA GCC AAA CAA CTG GGG GCA ACA GAC TCC ACA AAG ATA Ile Lys Glu Lys Ala Lys Gln Leu Gly Ala Thr Asp Ser Thr Lys Ile 3155 3160 3165	9864
TCA AAG GAG GTT GGC GCG AAA GTG TAT TCT ATG AAG CTG AGT AAC TGG Ser Lys Glu Val Gly Ala Lys Val Tyr Ser Met Lys Leu Ser Asn Trp 3170 3175 3180	9912
GTG ATA CAA GAA GAG AAT AAA CAA GGC AGC CTT GCC CCC CTG TTT GAA Val Ile Gln Glu Glu Asn Lys Gln Gly Ser Leu Ala Pro Leu Phe Glu 3185 3190 3195	9960
GAG CTC CTG CAA CAG TGC CCA CCC GGG GGC CAG AAC AAA ACC ACA CAT Glu Leu Leu Gln Gln Cys Pro Pro Gly Gly Gln Asn Lys Thr Thr His 3200 3205 3210 3215	10008
ATG GTC TCA GCC TAC CAA CTA GCT CAA GGG AAT TGG GTG CCA GTT AGT Met Val Ser Ala Tyr Gln Leu Ala Gln Gly Asn Trp Val Pro Val Ser 3220 3225 3230	10056
TGC CAC GTG TTC ATG GGG ACC ATA CCC GCC AGA AGA ACC AAG ACT CAT Cys His Val Phe Met Gly Thr Ile Pro Ala Arg Arg Thr Lys Thr His 3235 3240 3245	10104
CCT TAT GAG GCA TAC GTT AAG CTA AGG GAG TTG GTA GAT GAA CAT AAG Pro Tyr Glu Ala Tyr Val Lys Leu Arg Glu Leu Val Asp Glu His Lys 3250 3255 3260	10152
ATG AAG GCA TTA TGT GGC GGA TCA GGC CTA AGT AAG CAC AAC GAA TGG Met Lys Ala Leu Cys Gly Gly Ser Gly Leu Ser Lys His Asn Glu Trp 3265 3270 3275	10200
GTA ATT GGC AAG GTC AAG TAT CAA GGA AAC CTG AGG ACC AAA CAC ATG Val Ile Gly Lys Val Lys Tyr Gln Gly Asn Leu Arg Thr Lys His Met 3280 3285 3290 3295	10248
TTG AAC CCC GGA AAG GTG GCG GAG CAA CTG CAC AGA GAA GGG TAC AGG Leu Asn Pro Gly Lys Val Ala Glu Gln Leu His Arg Glu Gly Tyr Arg 3300 3305 3310	10296
CAC AAT GTG TAT AAT AAG ACA ATA GGT TCA GTG ATG ACA GCA ACT GGT His Asn Val Tyr Asn Lys Thr Ile Gly Ser Val Met Thr Ala Thr Gly 3315 3320 3325	10344
ATC AGG CTG GAG AAG TTA CCT GTG GTT AGG GCC CAA ACA GAC ACA ACC Ile Arg Leu Glu Lys Leu Pro Val Val Arg Ala Gln Thr Asp Thr Thr 3330 3335 3340	10392

AAC TTC CAC CAA GCA ATA AGG GAT AAA ATA GAC AAG GAG GAG AAC CTA Asn Phe His Gln Ala Ile Arg Asp Lys Ile Asp Lys Glu Glu Asn Leu 3345 3350 3355	10440
CAG ACC CCT GGC TTG CAT AAG AAG TTA ATG GAA GTC TTC AAT GCA TTA Gln Thr Pro Gly Leu His Lys Lys Leu Met Glu Val Phe Asn Ala Leu 3360 3365 3370 3375	10488
AAA AGA CCC GAG CTT GAG GCC TCT TAT GAC GCT GTG GAT TGG GAG GAA Lys Arg Pro Glu Leu Glu Ala Ser Tyr Asp Ala Val Asp Trp Glu Glu 3380 3385 3390	10536
TTG GAG AGA GGA ATA AAT AGG AAG GGT GCT GCT GGT TTC TTC GAA CGC Leu Glu Arg Gly Ile Asn Arg Lys Gly Ala Ala Gly Phe Phe Glu Arg 3395 3400 3405	10584
AAG AAC ATA GGA GAG GTT TTG GAT TCG GAA AAA AAT AAA GTC GAA GAG Lys Asn Ile Gly Glu Val Leu Asp Ser Glu Lys Asn Lys Val Glu Glu 3410 3415 3420	10632
GTT ATT GAC AGT TTG AAA AAA GGT AGG AAT ATC AGA TAC TAC GAA ACT Val Ile Asp Ser Leu Lys Lys Gly Arg Asn Ile Arg Tyr Tyr Glu Thr 3425 3430 3435	10680
GCA ATC CCG AAA AAC GAG AAG AGG GAT GTC AAT GAT GAC TGG ACC GCT Ala Ile Pro Lys Asn Glu Lys Arg Asp Val Asn Asp Asp Trp Thr Ala 3440 3445 3450 3455	10728
GGT GAC TTC GTA GAT GAG AAG AAG CCA AGA GTG ATA CAA TAC CCT GAG Gly Asp Phe Val Asp Glu Lys Lys Pro Arg Val Ile Gln Tyr Pro Glu 3460 3465 3470	10776
GCT AAA ACT AGG TTG GCT ATT ACT AAG GTA ATG TAC AAG TGG GTC AAA Ala Lys Thr Arg Leu Ala Ile Thr Lys Val Met Tyr Lys Trp Val Lys 3475 3480 3485	10824
CAG AAG CCA GTT GTC ATA CCG GGT TAT GAA GGT AAG ACA CCC CTG TTT Gln Lys Pro Val Val Ile Pro Gly Tyr Glu Gly Lys Thr Pro Leu Phe 3490 3495 3500	10872
CAA ATT TTT GAC AAA GTG AAG AAA GAA TGG GAT CAA TTC CAA AAC CCT Gln Ile Phe Asp Lys Val Lys Lys Glu Trp Asp Gln Phe Gln Asn Pro 3505 3510 3515	10920
GTG GCA GTT AGC TTT GAT ACC AAA GCG TGG GAT ACC CAG GTA ACC ACA Val Ala Val Ser Phe Asp Thr Lys Ala Trp Asp Thr Gln Val Thr Thr 3520 3525 3530 3535	10968
AGG GAT TTG GAG CTA ATA AGG GAT ATA CAG AAG TTC TAT TTT AAA AAG Arg Asp Leu Glu Leu Ile Arg Asp Ile Gln Lys Phe Tyr Phe Lys Lys 3540 3545 3550	11016
AAA TGG CAC AAA TTC ATT GAC ACC CTA ACC AAG CAC ATG TCA GAA GTA Lys Trp His Lys Phe Ile Asp Thr Leu Thr Lys His Met Ser Glu Val 3555 3560 3565	11064

CCC	GTA	ATC	AGT	GCC	GAC	GGG	GAG	GTA	TAC	ATA	AGG	AAA	GGT	CAG	AGA	11112
Pro	Val	Ile	Ser	Ala	Asp	Gly	Glu	Val	Tyr	Ile	Arg	Lys	Gly	Gln	Arg	
				3570				3575					3580			
GGC	AGT	GGG	CAA	CCT	GAC	ACG	AGC	GCA	GGC	AAC	AGC	ATG	TTG	AAT	GTG	11160
Gly	Ser	Gly	Gln	Pro	Asp	Thr	Ser	Ala	Gly	Asn	Ser	Met	Leu	Asn	Val	
		3585					3590				3595					
TTG	ACA	ATG	GTG	TAT	GCC	TTC	TGC	GAG	GCC	ACG	GGG	GTA	CCC	TAC	AAG	11208
Leu	Thr	Met	Val	Tyr	Ala	Phe	Cys	Glu	Ala	Thr	Gly	Val	Pro	Tyr	Lys	
		3600				3605				3610					3615	
AGT	TTT	GAC	AGA	GTG	GCA	AAG	ATC	CAT	GTC	TGC	GGG	GAT	GAT	GGT	TTC	11256
Ser	Phe	Asp	Arg	Val	Ala	Lys	Ile	His	Val	Cys	Gly	Asp	Asp	Gly	Phe	
				3620					3625					3630		
CTG	ATT	ACC	GAA	AGA	GCT	CTC	GGT	GAG	AAA	TTT	GCG	AGT	AAA	GGA	GTC	11304
Leu	Ile	Thr	Glu	Arg	Ala	Leu	Gly	Glu	Lys	Phe	Ala	Ser	Lys	Gly	Val	
			3635					3640					3645			
CAG	ATC	CTA	TAC	GAA	GCT	GGG	AAG	CCT	CAA	AAG	ATC	ACT	GAA	GGG	GAC	11352
Gln	Ile	Leu	Tyr	Glu	Ala	Gly	Lys	Pro	Gln	Lys	Ile	Thr	Glu	Gly	Asp	
		3650					3655					3660				
AAG	ATG	AAA	GTA	GCC	TAT	CAG	TTT	GAT	GAT	ATC	GAG	TTC	TGC	TCC	CAT	11400
Lys	Met	Lys	Val	Ala	Tyr	Gln	Phe	Asp	Asp	Ile	Glu	Phe	Cys	Ser	His	
		3665				3670					3675					
ACA	CCA	GTA	CAA	GTG	AGG	TGG	TCA	GAC	AAT	ACT	TCC	AGC	TAC	ATG	CCG	11448
Thr	Pro	Val	Gln	Val	Arg	Trp	Ser	Asp	Asn	Thr	Ser	Ser	Tyr	Met	Pro	
		3680			3685					3690					3695	
GGA	AGG	AAC	ACG	ACT	ACA	ATC	CTG	GCT	AAA	ATG	GCT	ACA	AGG	TTG	GAT	11496
Gly	Arg	Asn	Thr	Thr	Thr	Ile	Leu	Ala	Lys	Met	Ala	Thr	Arg	Leu	Asp	
				3700					3705					3710		
TCC	AGT	GGT	GAG	AGG	GGT	ACT	ATA	GCA	TAT	GAG	AAG	GCA	GTG	GCG	TTC	11544
Ser	Ser	Gly	Glu	Arg	Gly	Thr	Ile	Ala	Tyr	Glu	Lys	Ala	Val	Ala	Phe	
			3715					3720					3725			
AGC	TTT	TTG	TTG	ATG	TAC	TCC	TGG	AAC	CCA	CTG	ATC	AGA	AGG	ATA	TGC	11592
Ser	Phe	Leu	Leu	Met	Tyr	Ser	Trp	Asn	Pro	Leu	Ile	Arg	Arg	Ile	Cys	
		3730					3735					3740				
TTA	CTG	GTG	TTG	TCA	ACT	GAG	TTG	CAA	GTG	AGA	CCA	GGG	AAG	TCA	ACC	11640
Leu	Leu	Val	Leu	Ser	Thr	Glu	Leu	Gln	Val	Arg	Pro	Gly	Lys	Ser	Thr	
		3745				3750					3755					
ACC	TAT	TAC	TAT	GAA	GGG	GAC	CCA	ATA	TCC	GCT	TAC	AAG	GAA	GTC	ATT	11688
Thr	Tyr	Tyr	Tyr	Glu	Gly	Asp	Pro	Ile	Ser	Ala	Tyr	Lys	Glu	Val	Ile	
		3760			3765				3770					3775		
GGC	CAC	AAT	CTC	TTT	GAC	CTT	AAA	AGA	ACA	AGC	TTC	GAA	AAG	CTA	GCA	11736
Gly	His	Asn	Leu	Phe	Asp	Leu	Lys	Arg	Thr	Ser	Phe	Glu	Lys	Leu	Ala	
				3780					3785					3790		

AAG TTA AAT CTC AGC ATG TCC ACG CTC GGG GTG TGG ACT AGA CAC ACT 11784
 Lys Leu Asn Leu Ser Met Ser Thr Leu Gly Val Trp Thr Arg His Thr
 3795 3800 3805

AGC AAG AGA TTA CTA CAA GAT TGT GTC AAT GTT GGC ACC AAA GAG GGC 11832
 Ser Lys Arg Leu Leu Gln Asp Cys Val Asn Val Gly Thr Lys Glu Gly
 3810 3815 3820

AAC TGG CTG GTC AAT GCA GAC AGA CTA GTG AGT AGT AAG ACA GGA AAC 11880
 Asn Trp Leu Val Asn Ala Asp Arg Leu Val Ser Ser Lys Thr Gly Asn
 3825 3830 3835

AGG TAT ATA CCT GGA GAG GGC CAC ACC CTA CAA GGG AAA CAT TAT GAA 11928
 Arg Tyr Ile Pro Gly Glu Gly His Thr Leu Gln Gly Lys His Tyr Glu
 3840 3845 3850 3855

GAA CTG ATA CTG GCA AGG AAA CCG ATC GGT AAC TTT GAA GGG ACC GAT 11976
 Glu Leu Ile Leu Ala Arg Lys Pro Ile Gly Asn Phe Glu Gly Thr Asp
 3860 3865 3870

AGG TAT AAC TTG GGG CCA ATA GTC AAT GTA GTG TTG AGG AGA CTA AAA 12024
 Arg Tyr Asn Leu Gly Pro Ile Val Asn Val Val Leu Arg Arg Leu Lys
 3875 3880 3885

ATT ATG ATG ATG GCC CTG ATA GGA AGG GGG GTG TGAGCATGGT TGGCCCTTGA 12077
 Ile Met Met Met Ala Leu Ile Gly Arg Gly Val
 3890 3895

TCGGGCCCTA TCAGTAGAAC CCTATTGTAA ATAACATTAA CTTATTAATT ATTTAGATAC 12137

TATTATTTAT TTATTTATTT ATTTATTGAA TGAGCAAGTA CTGGTACAAA CTACCTCATG 12197

TTACCACACT ACACTCATTT TAACAGCACT TTAGCTGGAG GGAAAACCCT GACGTCCACA 12257

GTTGGACTAA GGTAATTTCC TAACGGC 12284

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3898 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Glu Leu Asn His Phe Glu Leu Leu Tyr Lys Thr Ser Lys Gln Lys
 1 5 10 15
 Pro Val Gly Val Glu Glu Pro Val Tyr Asp Thr Ala Gly Arg Pro Leu
 20 25 30

50

Phe Gly Asn Pro Ser Glu Val His Pro Gln Ser Thr Leu Lys Leu Pro
 35 40 45
 His Asp Arg Gly Arg Gly Asp Ile Arg Thr Thr Leu Arg Asp Leu Pro
 50 55 60
 Arg Lys Gly Asp Cys Arg Ser Gly Asn His Leu Gly Pro Val Ser Gly
 65 70 75 80
 Ile Tyr Ile Lys Pro Gly Pro Val Tyr Tyr Gln Asp Tyr Thr Gly Pro
 85 90 95
 Val Tyr His Arg Ala Pro Leu Glu Phe Phe Asp Glu Ala Gln Phe Cys
 100 105 110
 Glu Val Thr Lys Arg Ile Gly Arg Val Thr Gly Ser Asp Gly Lys Leu
 115 120 125
 Tyr His Ile Tyr Val Cys Val Asp Gly Cys Ile Leu Leu Lys Leu Ala
 130 135 140
 Lys Arg Gly Thr Pro Arg Thr Leu Lys Trp Ile Arg Asn Phe Thr Asn
 145 150 155 160
 Cys Pro Leu Trp Val Thr Ser Cys Ser Asp Asp Gly Ala Ser Gly Ser
 165 170 175
 Lys Asp Lys Lys Pro Asp Arg Met Asn Lys Gly Lys Leu Lys Ile Ala
 180 185 190
 Pro Arg Glu His Glu Lys Asp Ser Lys Thr Lys Pro Pro Asp Ala Thr
 195 200 205
 Ile Val Val Glu Gly Val Lys Tyr Gln Ile Lys Lys Lys Gly Lys Val
 210 215 220
 Lys Gly Lys Asn Thr Gln Asp Gly Leu Tyr His Asn Lys Asn Lys Pro
 225 230 235 240
 Pro Glu Ser Arg Lys Lys Leu Glu Lys Ala Leu Leu Ala Trp Ala Val
 245 250 255
 Ile Thr Ile Leu Leu Tyr Gln Pro Val Ala Ala Glu Asn Ile Thr Gln
 260 265 270
 Trp Asn Leu Ser Asp Asn Gly Thr Asn Gly Ile Gln Arg Ala Met Tyr
 275 280 285
 Leu Arg Gly Val Asn Arg Ser Leu His Gly Ile Trp Pro Glu Lys Ile
 290 295 300
 Cys Lys Gly Val Pro Thr His Leu Ala Thr Asp Thr Glu Leu Lys Glu
 305 310 315 320
 Ile Arg Gly Met Met Asp Ala Ser Glu Arg Thr Asn Tyr Thr Cys Cys
 325 330 335

Arg Leu Gln Arg His Glu Trp Asn Lys His Gly Trp Cys Asn Trp Tyr
 340 345 350
 Asn Ile Asp Pro Trp Ile Gln Leu Met Asn Arg Thr Gln Thr Asn Leu
 355 360 365
 Thr Glu Gly Pro Pro Asp Lys Glu Cys Ala Val Thr Cys Arg Tyr Asp
 370 375 380
 Lys Asn Thr Asp Val Asn Val Val Thr Gln Ala Arg Asn Arg Pro Thr
 385 390 395 400
 Thr Leu Thr Gly Cys Lys Lys Gly Lys Asn Phe Ser Phe Ala Gly Thr
 405 410 415
 Val Ile Glu Gly Pro Cys Asn Phe Asn Val Ser Val Glu Asp Ile Leu
 420 425 430
 Tyr Gly Asp His Glu Cys Gly Ser Leu Leu Gln Asp Thr Ala Leu Tyr
 435 440 445
 Leu Leu Asp Gly Met Thr Asn Thr Ile Glu Asn Ala Arg Gln Gly Ala
 450 455 460
 Ala Arg Val Thr Ser Trp Leu Gly Arg Gln Leu Ser Thr Ala Gly Lys
 465 470 475 480
 Lys Leu Glu Arg Arg Ser Lys Thr Trp Phe Gly Ala Tyr Ala Leu Ser
 485 490 495
 Pro Tyr Cys Asn Val Thr Arg Lys Ile Gly Tyr Ile Trp Tyr Thr Asn
 500 505 510
 Asn Cys Thr Pro Ala Cys Leu Pro Lys Asn Thr Lys Ile Ile Gly Pro
 515 520 525
 Gly Lys Phe Asp Thr Asn Ala Glu Asp Gly Lys Ile Leu His Glu Met
 530 535 540
 Gly Gly His Leu Ser Glu Phe Leu Leu Leu Ser Leu Val Ile Leu Ser
 545 550 555 560
 Asp Phe Ala Pro Glu Thr Ala Ser Thr Leu Tyr Leu Ile Leu His Tyr
 565 570 575
 Ala Ile Pro Gln Ser His Glu Glu Pro Glu Gly Cys Asp Thr Asn Gln
 580 585 590
 Leu Asn Leu Thr Val Lys Leu Arg Thr Glu Asp Val Val Pro Ser Ser
 595 600 605
 Val Trp Asn Ile Gly Lys Tyr Val Cys Val Arg Pro Asp Trp Trp Pro
 610 615 620

Tyr Glu Thr Lys Val Ala Leu Leu Phe Glu Glu Ala Gly Gln Val Ile
 625 630 635 640
 Lys Leu Val Leu Arg Ala Leu Arg Asp Leu Thr Arg Val Trp Asn Ser
 645 650 655
 Ala Ser Thr Thr Ala Phe Leu Ile Cys Leu Ile Lys Val Leu Arg Gly
 660 665 670
 Gln Val Val Gln Gly Ile Ile Trp Leu Leu Leu Val Thr Gly Ala Gln
 675 680 685
 Gly Arg Leu Ala Cys Lys Glu Asp Tyr Arg Tyr Ala Ile Ser Ser Thr
 690 695 700
 Asn Glu Ile Gly Leu Leu Gly Ala Glu Gly Leu Thr Thr Thr Trp Lys
 705 710 715 720
 Glu Tyr Ser His Gly Leu Gln Leu Asp Asp Gly Thr Val Lys Ala Val
 725 730 735
 Cys Thr Ala Gly Ser Phe Lys Val Thr Ala Leu Asn Val Val Ser Arg
 740 745 750
 Arg Tyr Leu Ala Ser Leu His Lys Arg Ala Leu Pro Thr Ser Val Thr
 755 760 765
 Phe Glu Leu Leu Phe Asp Gly Thr Asn Pro Ala Ile Glu Glu Met Asp
 770 775 780
 Asp Asp Phe Gly Phe Gly Leu Cys Pro Phe Asp Thr Ser Pro Val Ile
 785 790 795 800
 Lys Gly Lys Tyr Asn Thr Thr Leu Leu Asn Gly Ser Ala Phe Tyr Leu
 805 810 815
 Val Cys Pro Ile Gly Trp Thr Gly Val Val Glu Cys Thr Ala Val Ser
 820 825 830
 Pro Thr Thr Leu Arg Thr Glu Val Val Lys Thr Phe Arg Arg Asp Lys
 835 840 845
 Pro Phe Pro His Arg Val Asp Cys Val Thr Thr Ile Val Glu Lys Glu
 850 855 860
 Asp Leu Phe His Cys Lys Leu Gly Gly Asn Trp Thr Cys Val Lys Gly
 865 870 875 880
 Asp Pro Val Thr Tyr Lys Gly Gly Gln Val Lys Gln Cys Arg Trp Cys
 885 890 895
 Gly Phe Glu Phe Lys Glu Pro Tyr Gly Leu Pro His Tyr Pro Ile Gly
 900 905 910
 Lys Cys Ile Leu Thr Asn Glu Thr Gly Tyr Arg Val Val Asp Ser Thr
 915 920 925

Asp Cys Asn Arg Asp Gly Val Val Ile Ser Thr Glu Gly Glu His Glu
 930 935 940
 Cys Leu Ile Gly Asn Thr Thr Val Lys Val His Ala Leu Asp Glu Arg
 945 950 955 960
 Leu Gly Pro Met Pro Cys Arg Pro Lys Glu Ile Val Ser Ser Glu Gly
 965 970 975
 Pro Val Arg Lys Thr Ser Cys Thr Phe Asn Tyr Thr Lys Thr Leu Arg
 980 985 990
 Asn Lys Tyr Tyr Glu Pro Arg Asp Ser Tyr Phe Gln Gln Tyr Met Leu
 995 1000 1005
 Lys Gly Glu Tyr Gln Tyr Trp Phe Asn Leu Asp Val Thr Asp His His
 1010 1015 1020
 Thr Asp Tyr Phe Ala Glu Phe Val Val Leu Val Val Val Ala Leu Leu
 1025 1030 1035 1040
 Gly Gly Arg Tyr Val Leu Trp Leu Ile Val Thr Tyr Ile Ile Leu Thr
 1045 1050 1055
 Glu Gln Leu Ala Ala Gly Leu Gln Leu Gly Gln Gly Glu Val Val Leu
 1060 1065 1070
 Ile Gly Asn Leu Ile Thr His Thr Asp Asn Glu Val Val Val Tyr Phe
 1075 1080 1085
 Leu Leu Leu Tyr Leu Val Ile Arg Asp Glu Pro Ile Lys Lys Trp Ile
 1090 1095 1100
 Leu Leu Leu Phe His Ala Met Thr Asn Asn Pro Val Lys Thr Ile Thr
 1105 1110 1115 1120
 Val Ala Leu Leu Met Ile Ser Gly Val Ala Lys Gly Gly Lys Ile Asp
 1125 1130 1135
 Gly Gly Trp Gln Arg Gln Pro Val Thr Ser Phe Asp Ile Gln Leu Ala
 1140 1145 1150
 Leu Ala Val Val Val Val Val Val Met Leu Leu Ala Lys Arg Asp Pro
 1155 1160 1165
 Thr Thr Phe Pro Leu Val Ile Thr Val Ala Thr Leu Arg Thr Ala Lys
 1170 1175 1180
 Ile Thr Asn Gly Phe Ser Thr Asp Leu Val Ile Ala Thr Val Ser Ala
 1185 1190 1195 1200
 Ala Leu Leu Thr Trp Thr Tyr Ile Ser Asp Tyr Tyr Lys Tyr Lys Thr
 1205 1210 1215

Trp Leu Gln Tyr Leu Val Ser Thr Val Thr Gly Ile Phe Leu Ile Arg
 1220 1225 1230
 Val Leu Lys Gly Ile Gly Glu Leu Asp Leu His Ala Pro Thr Leu Pro
 1235 1240 1245
 Ser His Arg Pro Leu Phe Tyr Ile Leu Val Tyr Leu Ile Ser Thr Ala
 1250 1255 1260
 Val Val Thr Arg Trp Asn Leu Asp Val Ala Gly Leu Leu Leu Gln Cys
 1265 1270 1275 1280
 Val Pro Thr Leu Leu Met Val Phe Thr Met Trp Ala Asp Ile Leu Thr
 1285 1290 1295
 Leu Ile Leu Ile Leu Pro Thr Tyr Glu Leu Thr Lys Leu Tyr Tyr Leu
 1300 1305 1310
 Lys Glu Val Lys Ile Gly Ala Glu Arg Gly Trp Leu Trp Lys Thr Asn
 1315 1320 1325
 Tyr Lys Arg Val Asn Asp Ile Tyr Glu Val Asp Gln Thr Ser Glu Gly
 1330 1335 1340
 Val Tyr Leu Phe Pro Ser Lys Gln Arg Thr Ser Ala Ile Thr Ser Thr
 1345 1350 1355 1360
 Met Leu Pro Leu Ile Lys Ala Ile Leu Ile Ser Cys Ile Ser Asn Lys
 1365 1370 1375
 Trp Gln Leu Ile Tyr Leu Leu Tyr Leu Ile Phe Glu Val Ser Tyr Tyr
 1380 1385 1390
 Leu His Lys Lys Val Ile Asp Glu Ile Ala Gly Gly Thr Asn Phe Val
 1395 1400 1405
 Ser Arg Leu Val Ala Ala Leu Ile Glu Val Asn Trp Ala Phe Asp Asn
 1410 1415 1420
 Glu Glu Val Lys Gly Leu Lys Lys Phe Phe Leu Leu Ser Ser Arg Val
 1425 1430 1435 1440
 Lys Glu Leu Ile Ile Lys His Lys Val Arg Asn Glu Val Val Val Arg
 1445 1450 1455
 Trp Phe Gly Asp Glu Glu Ile Tyr Gly Met Pro Lys Leu Ile Gly Leu
 1460 1465 1470
 Val Lys Ala Ala Thr Leu Ser Arg Asn Lys His Cys Met Leu Cys Thr
 1475 1480 1485
 Val Cys Glu Asp Arg Asp Trp Arg Gly Glu Thr Cys Pro Lys Cys Gly
 1490 1495 1500
 Arg Phe Gly Pro Pro Val Val Cys Gly Met Thr Leu Ala Asp Phe Glu
 1505 1510 1515 1520

Glu Lys His Tyr Lys Arg Ile Phe Ile Arg Glu Asp Gln Ser Gly Gly
 1525 1530 1535
 Pro Leu Arg Glu Glu His Ala Gly Tyr Leu Gln Tyr Lys Ala Arg Gly
 1540 1545 1550
 Gln Leu Phe Leu Arg Asn Leu Pro Val Leu Ala Thr Lys Val Lys Met
 1555 1560 1565
 Leu Leu Val Gly Asn Leu Gly Thr Glu Ile Gly Asp Leu Glu His Leu
 1570 1575 1580
 Gly Trp Val Leu Arg Gly Pro Ala Val Cys Lys Lys Val Thr Glu His
 1585 1590 1595 1600
 Glu Arg Cys Thr Thr Ser Ile Met Asp Lys Leu Thr Ala Phe Phe Gly
 1605 1610 1615
 Val Met Pro Arg Gly Thr Thr Pro Arg Ala Pro Val Arg Phe Pro Thr
 1620 1625 1630
 Ser Leu Leu Lys Ile Arg Arg Gly Leu Glu Thr Gly Trp Ala Tyr Thr
 1635 1640 1645
 His Gln Gly Gly Ile Ser Ser Val Asp His Val Thr Cys Gly Lys Asp
 1650 1655 1660
 Leu Leu Val Cys Asp Thr Met Gly Arg Thr Arg Val Val Cys Gln Ser
 1665 1670 1675 1680
 Asn Asn Lys Met Thr Asp Glu Ser Glu Tyr Gly Val Lys Thr Asp Ser
 1685 1690 1695
 Gly Cys Pro Glu Gly Ala Arg Cys Tyr Val Phe Asn Pro Glu Ala Val
 1700 1705 1710
 Asn Ile Ser Gly Thr Lys Gly Ala Met Val His Leu Gln Lys Thr Gly
 1715 1720 1725
 Gly Glu Phe Thr Cys Val Thr Ala Ser Gly Thr Pro Ala Phe Phe Asp
 1730 1735 1740
 Leu Lys Asn Leu Lys Gly Trp Ser Gly Leu Pro Ile Phe Glu Ala Ser
 1745 1750 1755 1760
 Ser Gly Arg Val Val Gly Arg Val Lys Val Gly Lys Asn Glu Asp Ser
 1765 1770 1775
 Lys Pro Thr Lys Leu Met Ser Gly Ile Gln Thr Val Ser Lys Ser Ala
 1780 1785 1790
 Thr Asp Leu Thr Glu Met Val Lys Lys Ile Thr Thr Met Asn Arg Gly
 1795 1800 1805

56

Glu Phe Arg Gln Ile Thr Leu Ala Thr Gly Ala Gly Lys Thr Thr Glu
 1810 1815 1820
 Leu Pro Arg Ser Val Ile Glu Glu Ile Gly Arg His Lys Arg Val Leu
 1825 1830 1835 1840
 Val Leu Ile Pro Leu Arg Ala Ala Ala Glu Ser Val Tyr Gln Tyr Met
 1845 1850 1855
 Arg Gln Lys His Pro Ser Ile Ala Phe Asn Leu Arg Ile Gly Glu Met
 1860 1865 1870
 Lys Glu Gly Asp Met Ala Thr Gly Ile Thr Tyr Ala Ser Tyr Gly Tyr
 1875 1880 1885
 Phe Cys Gln Met Ser Gln Pro Lys Leu Arg Ala Ala Met Val Glu Tyr
 1890 1895 1900
 Ser Phe Ile Phe Leu Asp Glu Tyr His Cys Ala Thr Pro Glu Gln Leu
 1905 1910 1915 1920
 Ala Ile Met Gly Lys Ile His Arg Phe Ser Glu Asn Leu Arg Val Val
 1925 1930 1935
 Ala Met Thr Ala Thr Pro Ala Gly Thr Val Thr Thr Thr Gly Gln Lys
 1940 1945 1950
 His Pro Ile Glu Glu Phe Ile Ala Pro Glu Val Met Lys Gly Glu Asp
 1955 1960 1965
 Leu Gly Ser Glu Tyr Leu Asp Ile Ala Gly Leu Lys Ile Pro Val Glu
 1970 1975 1980
 Glu Met Lys Asn Asn Met Leu Val Phe Val Pro Thr Arg Asn Met Ala
 1985 1990 1995 2000
 Val Glu Ala Ala Lys Lys Leu Lys Ala Lys Gly Tyr Asn Ser Gly Tyr
 2005 2010 2015
 Tyr Tyr Ser Gly Glu Asp Pro Ser Asn Leu Arg Val Val Thr Ser Gln
 2020 2025 2030
 Ser Pro Tyr Val Val Val Ala Thr Asn Ala Ile Glu Ser Gly Val Thr
 2035 2040 2045
 Leu Pro Asp Leu Asp Val Val Val Asp Thr Gly Leu Lys Cys Glu Lys
 2050 2055 2060
 Arg Ile Arg Leu Ser Pro Lys Met Pro Phe Ile Val Thr Gly Leu Lys
 2065 2070 2075 2080
 Arg Met Ala Val Thr Ile Gly Glu Gln Ala Gln Arg Arg Gly Arg Val
 2085 2090 2095
 Gly Arg Val Lys Pro Gly Arg Tyr Tyr Arg Ser Gln Glu Thr Pro Val
 2100 2105 2110

57

Gly Ser Lys Asp Tyr His Tyr Asp Leu Leu Gln Ala Gln Arg Tyr Gly
 2115 2120 2125
 Ile Glu Asp Gly Ile Asn Ile Thr Lys Ser Phe Arg Glu Met Asn Tyr
 2130 2135 2140
 Asp Trp Ser Leu Tyr Glu Glu Asp Ser Leu Met Ile Thr Gln Leu Glu
 2145 2150 2155 2160
 Ile Leu Asn Asn Leu Leu Ile Ser Glu Glu Leu Pro Met Ala Val Lys
 2165 2170 2175
 Asn Ile Met Ala Arg Thr Asp His Pro Glu Pro Ile Gln Leu Ala Tyr
 2180 2185 2190
 Asn Ser Tyr Glu Thr Gln Val Pro Val Leu Phe Pro Lys Ile Arg Asn
 2195 2200 2205
 Gly Glu Val Thr Asp Thr Tyr Asp Asn Tyr Thr Phe Leu Asn Ala Arg
 2210 2215 2220
 Lys Leu Gly Asp Asp Val Pro Pro Tyr Val Tyr Ala Thr Glu Asp Glu
 2225 2230 2235 2240
 Asp Leu Ala Val Glu Leu Leu Gly Leu Asp Trp Pro Asp Pro Gly Asn
 2245 2250 2255
 Gln Gly Thr Val Glu Ala Gly Arg Ala Leu Lys Gln Val Val Gly Leu
 2260 2265 2270
 Ser Thr Ala Glu Asn Ala Leu Leu Val Ala Leu Phe Gly Tyr Val Gly
 2275 2280 2285
 Tyr Gln Ala Leu Ser Lys Arg His Ile Pro Val Val Thr Asp Ile Tyr
 2290 2295 2300
 Ser Val Glu Asp His Arg Leu Glu Asp Thr Thr His Leu Gln Tyr Ala
 2305 2310 2315 2320
 Pro Asn Ala Ile Lys Thr Glu Gly Lys Glu Thr Glu Leu Lys Glu Leu
 2325 2330 2335
 Ala Gln Gly Asp Val Gln Arg Cys Val Glu Ala Val Thr Asn Tyr Ala
 2340 2345 2350
 Arg Glu Gly Ile Gln Phe Met Lys Ser Gln Ala Leu Lys Val Arg Glu
 2355 2360 2365
 Thr Pro Thr Tyr Lys Glu Thr Met Asn Thr Val Ala Asp Tyr Val Lys
 2370 2375 2380
 Lys Phe Ile Glu Ala Leu Thr Asp Ser Lys Glu Asp Ile Ile Lys Tyr
 2385 2390 2395 2400

Gly Leu Trp Gly Ala His Thr Ala Leu Tyr Lys Ser Ile Gly Ala Arg
 2405 2410 2415
 Leu Gly His Glu Thr Ala Phe Ala Thr Leu Val Val Lys Trp Leu Ala
 2420 2425 2430
 Phe Gly Gly Glu Ser Ile Ser Asp His Ile Lys Gln Ala Ala Thr Asp
 2435 2440 2445
 Leu Val Val Tyr Tyr Ile Ile Asn Arg Pro Gln Phe Pro Gly Asp Thr
 2450 2455 2460
 Glu Thr Gln Gln Glu Gly Arg Lys Phe Val Ala Ser Leu Leu Val Ser
 2465 2470 2475 2480
 Ala Leu Ala Thr Tyr Thr Tyr Lys Ser Trp Asn Tyr Asn Asn Leu Ser
 2485 2490 2495
 Lys Ile Val Glu Pro Ala Leu Ala Thr Leu Pro Tyr Ala Ala Lys Ala
 2500 2505 2510
 Leu Lys Leu Phe Ala Pro Thr Arg Leu Glu Ser Val Val Ile Leu Ser
 2515 2520 2525
 Thr Ala Ile Tyr Lys Thr Tyr Leu Ser Ile Arg Arg Gly Lys Ser Asp
 2530 2535 2540
 Gly Leu Leu Gly Thr Gly Val Ser Ala Ala Met Glu Ile Met Ser Gln
 2545 2550 2555 2560
 Asn Pro Val Ser Val Gly Ile Ala Val Met Leu Gly Val Gly Ala Val
 2565 2570 2575
 Ala Ala His Asn Ala Ile Glu Ala Ser Glu Gln Lys Arg Thr Leu Leu
 2580 2585 2590
 Met Lys Val Phe Val Lys Asn Phe Leu Asp Gln Ala Ala Thr Asp Glu
 2595 2600 2605
 Leu Val Lys Glu Ser Pro Glu Lys Ile Ile Met Ala Leu Phe Glu Ala
 2610 2615 2620
 Val Gln Thr Val Gly Asn Pro Leu Arg Leu Val Tyr His Leu Tyr Gly
 2625 2630 2635 2640
 Val Phe Tyr Lys Gly Trp Glu Ala Lys Glu Leu Ala Gln Arg Thr Ala
 2645 2650 2655
 Gly Arg Asn Leu Phe Thr Leu Ile Met Phe Glu Ala Val Glu Leu Leu
 2660 2665 2670
 Gly Val Asp Ser Glu Gly Lys Ile Arg Gln Leu Ser Ser Asn Tyr Ile
 2675 2680 2685
 Leu Glu Leu Leu Tyr Lys Phe Arg Asp Asn Ile Lys Ser Ser Val Arg
 2690 2695 2700

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Glu Ile Ala Ile Ser Trp Ala Pro Ala Pro Phe Ser Cys Asp Trp Thr
 2705 2710 2715 2720
 Pro Thr Asp Asp Arg Ile Gly Leu Pro His Asp Asn Tyr Leu Arg Val
 2725 2730 2735
 Glu Thr Lys Cys Pro Cys Gly Tyr Arg Met Lys Ala Val Lys Asn Cys
 2740 2745 2750
 Ala Gly Glu Leu Arg Leu Leu Glu Glu Gly Gly Ser Phe Leu Cys Arg
 2755 2760 2765
 Asn Lys Phe Gly Arg Gly Ser Gln Asn Tyr Arg Val Thr Lys Tyr Tyr
 2770 2775 2780
 Asp Asp Asn Leu Ser Glu Ile Lys Pro Val Ile Arg Met Glu Gly His
 2785 2790 2795 2800
 Val Glu Leu Tyr Tyr Lys Gly Ala Thr Ile Lys Leu Asp Phe Asn Asn
 2805 2810 2815
 Ser Lys Thr Val Leu Ala Thr Asp Lys Trp Glu Val Asp His Ser Thr
 2820 2825 2830
 Leu Val Arg Ala Leu Lys Arg Tyr Thr Gly Ala Gly Tyr Arg Gly Ala
 2835 2840 2845
 Tyr Leu Gly Glu Lys Pro Asn His Lys His Leu Ile Gln Arg Asp Cys
 2850 2855 2860
 Ala Thr Ile Thr Lys Asp Lys Val Cys Phe Ile Lys Met Lys Arg Gly
 2865 2870 2875 2880
 Cys Ala Phe Thr Tyr Asp Leu Ser Leu His Asn Leu Thr Arg Leu Ile
 2885 2890 2895
 Glu Leu Val His Lys Asn Asn Leu Glu Asp Arg Glu Ile Pro Ala Val
 2900 2905 2910
 Thr Val Thr Thr Trp Leu Ala Tyr Thr Phe Val Asn Glu Asp Ile Gly
 2915 2920 2925
 Thr Ile Lys Pro Thr Phe Gly Glu Lys Val Thr Pro Glu Lys Gln Glu
 2930 2935 2940
 Glu Val Val Leu Gln Pro Ala Val Val Val Asp Thr Thr Asp Val Ala
 2945 2950 2955 2960
 Val Thr Val Val Gly Glu Thr Ser Thr Met Thr Thr Gly Glu Thr Pro
 2965 2970 2975
 Thr Thr Phe Thr Ser Leu Gly Ser Asp Ser Lys Val Arg Gln Val Leu
 2980 2985 2990

Lys Leu Gly Val Asp Asp Gly Gln Tyr Pro Gly Pro Asn Gln Gln Arg
 2995 3000 3005
 Ala Ser Leu Leu Glu Ala Ile Gln Gly Val Asp Glu Arg Pro Ser Val
 3010 3015 3020
 Leu Ile Leu Gly Ser Asp Lys Ala Thr Ser Asn Arg Val Lys Thr Ala
 3025 3030 3035 3040
 Lys Asn Val Lys Ile Tyr Arg Ser Arg Asp Pro Leu Glu Leu Arg Glu
 3045 3050 3055
 Met Met Lys Arg Gly Lys Ile Leu Val Val Ala Leu Ser Arg Val Asp
 3060 3065 3070
 Thr Ala Leu Leu Lys Phe Val Asp Tyr Lys Gly Thr Phe Leu Thr Arg
 3075 3080 3085
 Glu Thr Leu Glu Ala Leu Ser Leu Gly Lys Pro Lys Lys Arg Asp Ile
 3090 3095 3100
 Thr Lys Ala Glu Ala Gln Trp Leu Leu Arg Leu Glu Asp Gln Ile Glu
 3105 3110 3115 3120
 Glu Leu Pro Asp Trp Phe Ala Ala Lys Glu Pro Ile Phe Leu Glu Ala
 3125 3130 3135
 Asn Ile Lys Arg Asp Lys Tyr His Leu Val Gly Asp Ile Ala Thr Ile
 3140 3145 3150
 Lys Glu Lys Ala Lys Gln Leu Gly Ala Thr Asp Ser Thr Lys Ile Ser
 3155 3160 3165
 Lys Glu Val Gly Ala Lys Val Tyr Ser Met Lys Leu Ser Asn Trp Val
 3170 3175 3180
 Ile Gln Glu Glu Asn Lys Gln Gly Ser Leu Ala Pro Leu Phe Glu Glu
 3185 3190 3195 3200
 Leu Leu Gln Gln Cys Pro Pro Gly Gly Gln Asn Lys Thr Thr His Met
 3205 3210 3215
 Val Ser Ala Tyr Gln Leu Ala Gln Gly Asn Trp Val Pro Val Ser Cys
 3220 3225 3230
 His Val Phe Met Gly Thr Ile Pro Ala Arg Arg Thr Lys Thr His Pro
 3235 3240 3245
 Tyr Glu Ala Tyr Val Lys Leu Arg Glu Leu Val Asp Glu His Lys Met
 3250 3255 3260
 Lys Ala Leu Cys Gly Gly Ser Gly Leu Ser Lys His Asn Glu Trp Val
 3265 3270 3275 3280
 Ile Gly Lys Val Lys Tyr Gln Gly Asn Leu Arg Thr Lys His Met Leu
 3285 3290 3295

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Asn Pro Gly Lys Val Ala Glu Gln Leu His Arg Glu Gly Tyr Arg His
 3300 3305 3310
 Asn Val Tyr Asn Lys Thr Ile Gly Ser Val Met Thr Ala Thr Gly Ile
 3315 3320 3325
 Arg Leu Glu Lys Leu Pro Val Val Arg Ala Gln Thr Asp Thr Thr Asn
 3330 3335 3340
 Phe His Gln Ala Ile Arg Asp Lys Ile Asp Lys Glu Glu Asn Leu Gln
 3345 3350 3355 3360
 Thr Pro Gly Leu His Lys Lys Leu Met Glu Val Phe Asn Ala Leu Lys
 3365 3370 3375
 Arg Pro Glu Leu Glu Ala Ser Tyr Asp Ala Val Asp Trp Glu Glu Leu
 3380 3385 3390
 Glu Arg Gly Ile Asn Arg Lys Gly Ala Ala Gly Phe Phe Glu Arg Lys
 3395 3400 3405
 Asn Ile Gly Glu Val Leu Asp Ser Glu Lys Asn Lys Val Glu Glu Val
 3410 3415 3420
 Ile Asp Ser Leu Lys Lys Gly Arg Asn Ile Arg Tyr Tyr Glu Thr Ala
 3425 3430 3435 3440
 Ile Pro Lys Asn Glu Lys Arg Asp Val Asn Asp Asp Trp Thr Ala Gly
 3445 3450 3455
 Asp Phe Val Asp Glu Lys Lys Pro Arg Val Ile Gln Tyr Pro Glu Ala
 3460 3465 3470
 Lys Thr Arg Leu Ala Ile Thr Lys Val Met Tyr Lys Trp Val Lys Gln
 3475 3480 3485
 Lys Pro Val Val Ile Pro Gly Tyr Glu Gly Lys Thr Pro Leu Phe Gln
 3490 3495 3500
 Ile Phe Asp Lys Val Lys Lys Glu Trp Asp Gln Phe Gln Asn Pro Val
 3505 3510 3515 3520
 Ala Val Ser Phe Asp Thr Lys Ala Trp Asp Thr Gln Val Thr Thr Arg
 3525 3530 3535
 Asp Leu Glu Leu Ile Arg Asp Ile Gln Lys Phe Tyr Phe Lys Lys Lys
 3540 3545 3550
 Trp His Lys Phe Ile Asp Thr Leu Thr Lys His Met Ser Glu Val Pro
 3555 3560 3565
 Val Ile Ser Ala Asp Gly Glu Val Tyr Ile Arg Lys Gly Gln Arg Gly
 3570 3575 3580

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Ser Gly Gln Pro Asp Thr Ser Ala Gly Asn Ser Met Leu Asn Val Leu
 3585 3590 3595 3600
 Thr Met Val Tyr Ala Phe Cys Glu Ala Thr Gly Val Pro Tyr Lys Ser
 3605 3610 3615
 Phe Asp Arg Val Ala Lys Ile His Val Cys Gly Asp Asp Gly Phe Leu
 3620 3625 3630
 Ile Thr Glu Arg Ala Leu Gly Glu Lys Phe Ala Ser Lys Gly Val Gln
 3635 3640 3645
 Ile Leu Tyr Glu Ala Gly Lys Pro Gln Lys Ile Thr Glu Gly Asp Lys
 3650 3655 3660
 Met Lys Val Ala Tyr Gln Phe Asp Asp Ile Glu Phe Cys Ser His Thr
 3665 3670 3675 3680
 Pro Val Gln Val Arg Trp Ser Asp Asn Thr Ser Ser Tyr Met Pro Gly
 3685 3690 3695
 Arg Asn Thr Thr Thr Ile Leu Ala Lys Met Ala Thr Arg Leu Asp Ser
 3700 3705 3710
 Ser Gly Glu Arg Gly Thr Ile Ala Tyr Glu Lys Ala Val Ala Phe Ser
 3715 3720 3725
 Phe Leu Leu Met Tyr Ser Trp Asn Pro Leu Ile Arg Arg Ile Cys Leu
 3730 3735 3740
 Leu Val Leu Ser Thr Glu Leu Gln Val Arg Pro Gly Lys Ser Thr Thr
 3745 3750 3755 3760
 Tyr Tyr Tyr Glu Gly Asp Pro Ile Ser Ala Tyr Lys Glu Val Ile Gly
 3765 3770 3775
 His Asn Leu Phe Asp Leu Lys Arg Thr Ser Phe Glu Lys Leu Ala Lys
 3780 3785 3790
 Leu Asn Leu Ser Met Ser Thr Leu Gly Val Trp Thr Arg His Thr Ser
 3795 3800 3805
 Lys Arg Leu Leu Gln Asp Cys Val Asn Val Gly Thr Lys Glu Gly Asn
 3810 3815 3820
 Trp Leu Val Asn Ala Asp Arg Leu Val Ser Ser Lys Thr Gly Asn Arg
 3825 3830 3835 3840
 Tyr Ile Pro Gly Glu Gly His Thr Leu Gln Gly Lys His Tyr Glu Glu
 3845 3850 3855
 Leu Ile Leu Ala Arg Lys Pro Ile Gly Asn Phe Glu Gly Thr Asp Arg
 3860 3865 3870
 Tyr Asn Leu Gly Pro Ile Val Asn Val Val Leu Arg Arg Leu Lys Ile
 3875 3880 3885

Met Met Met Ala Leu Ile Gly Arg Gly Val
3890 3895

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..33
- (D) OTHER INFORMATION: /label= primer_1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCTACTAACC ACGTTAAGTG CTGTGACTTT AAA

33

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..39
- (D) OTHER INFORMATION: /label= primer_2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TTCTGTTCTC AAGGTTGTGG GGCTCACTGC TGTGCACTC

39

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(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..16
- (D) OTHER INFORMATION: /label= Adaptor_1
/note= "Upper strand of Bam HI - Hinf I adaptor,
containing ATG at 364-366"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GATCCACCAT GGAGTT

16

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..16
- (D) OTHER INFORMATION: /label= Adaptor_2
/note= "Lower strand of Bam HI - Hinf I adaptor,
containing ATG at 364-366"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GTGGTACCTC AACTTA

16

65

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..10
- (D) OTHER INFORMATION: /label= Adaptor_3
/note= "Double stranded Stu I - Eco RI blunt adaptor"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCCTGAATTC

10

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /label= Adaptor_4
/note= "Upper strand of Bgl II - BamH I adaptor"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GATCCACCAT GGGGGCCCTG T

21

66

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..14
- (D) OTHER INFORMATION: /label= Adaptor_5
/note= "Lower strand of Bgl II - BamH I adaptor"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GTGGTACCCC CGGG

14

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..15
- (D) OTHER INFORMATION: /label= Adaptor_6
/note= "Upper strand of Ban I - Eco R I adaptor"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GTGCCTATGC CTGAG

15

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(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..15
- (D) OTHER INFORMATION: /label= Adaptor_7
/note= "Lower strand of Ban I - Eco R I adaptor"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GATACGGACT CTAA

15

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (B) CLONE: lambda gt11 clone

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..300
- (D) OTHER INFORMATION: /note= "Part of 0.8 kb insert of
Lambda gt11"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

AGT	GAC	AAC	GGC	ACT	AAT	GGT	ATT	CAG	CGA	GCC	ATG	TAT	CTT	AGA	GGG	48
Ser	Asp	Asn	Gly	Thr	Asn	Gly	Ile	Gln	Arg	Ala	Met	Tyr	Leu	Arg	Gly	
1				5				10						15		
GTT	AAC	AGG	AGC	TTA	CAT	GGG	ATC	TGG	CCC	GAG	AAA	ATA	TGC	AAG	GGG	96
Val	Asn	Arg	Ser	Leu	His	Gly	Ile	Trp	Pro	Glu	Lys	Ile	Cys	Lys	Gly	
			20				25					30				
GTC	CCC	ACT	CAT	CTG	GCC	ACT	GAC	ACG	GAA	CTG	AAA	GAG	ATA	CGC	GGG	144
Val	Pro	Thr	His	Leu	Ala	Thr	Asp	Thr	Glu	Leu	Lys	Glu	Ile	Arg	Gly	
			35				40					45				

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ATG	ATG	GAT	GCC	AGC	GAG	AGG	ACA	AAC	TAT	ACG	TGC	TGT	AGG	TTA	CAA	192
Met	Met	Asp	Ala	Ser	Glu	Arg	Thr	Asn	Tyr	Thr	Cys	Cys	Arg	Leu	Gln	
	50					55					60					
AGA	CAT	GAA	TGG	AAC	AAA	CAT	GGA	TGG	TGT	AAC	TGG	TAC	AAC	ATA	GAC	240
Arg	His	Glu	Trp	Asn	Lys	His	Gly	Trp	Cys	Asn	Trp	Tyr	Asn	Ile	Asp	
	65				70					75					80	
CCT	TGG	ATT	CAG	TTA	ATG	AAC	AGG	ACC	CAA	ACA	AAT	TTG	ACA	GAA	GGC	288
Pro	Trp	Ile	Gln	Leu	Met	Asn	Arg	Thr	Gln	Thr	Asn	Leu	Thr	Glu	Gly	
				85					90					95		
CCT	CCA	GAT	AAG													300
Pro	Pro	Asp	Lys													
			100													

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Ser	Asp	Asn	Gly	Thr	Asn	Gly	Ile	Gln	Arg	Ala	Met	Tyr	Leu	Arg	Gly	
1				5				10						15		
Val	Asn	Arg	Ser	Leu	His	Gly	Ile	Trp	Pro	Glu	Lys	Ile	Cys	Lys	Gly	
			20					25					30			
Val	Pro	Thr	His	Leu	Ala	Thr	Asp	Thr	Glu	Leu	Lys	Glu	Ile	Arg	Gly	
		35					40					45				
Met	Met	Asp	Ala	Ser	Glu	Arg	Thr	Asn	Tyr	Thr	Cys	Cys	Arg	Leu	Gln	
	50					55					60					
Arg	His	Glu	Trp	Asn	Lys	His	Gly	Trp	Cys	Asn	Trp	Tyr	Asn	Ile	Asp	
	65				70				75					80		
Pro	Trp	Ile	Gln	Leu	Met	Asn	Arg	Thr	Gln	Thr	Asn	Leu	Thr	Glu	Gly	
				85					90					95		
Pro	Pro	Asp	Lys													
			100													

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